

SEQUENCE LISTING

<110> McIntosh, J. Michael
 Olivera, Baldomero M.
 Cruz, Lourdes J.
 Corpuz, Gloria P.
 Jones, Robert M.
 Garrett, James E.

<120> Conotoxin Peptides

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<150> US 60/173,298

<151> 1999-12-28

<150> US 60/118,381

<151> 1999-01-29

<150> US 09/493,143

<151> 2000-01-28

<160> 20

<170> PatentIn Ver. 2.0

<210> 1

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:generic
 conotoxin peptide sequence

<220>

<221> PEPTIDE

<222> (1)..(2)

<223> Xaa at residue 1 is des-Xaa, Asn, Gln or pyro-Glu;
 Xaa at residue 2 is des-Xaa, Gly, Ala, Glu, gamma-
 carboxy-Glu, Asp, Asn, Ser, Thr, g-Asn (where g is
 glycosylation), g-Ser or g-Thr;

<220>

<221> PEPTIDE

<222> (3)..(7)

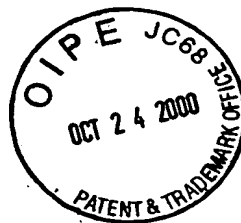
<223> Xaa at residue 3 is Val, Ala, Gly, Leu, Ile, Ser,
 Thr, g-Asn, g-Ser or g-Thr; Xaa at residue 7 is
 Phe, Tyr, meta-Tyr, ortho-Tyr, nor-Tyr,
 mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
 O-phospho-Tyr,

<220>

<221> PEPTIDE

<222> (7)

<223> nitro-Tyr, Trp (D or L), neo-Trp, halo-Trp (D or
 L), any synthetic aromatic amino acid, an
 aliphatic amino acid bearing linear or branched
 saturated hydrocarbon chains such as Leu (D or L),
 Ile and



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<220>
 <221> PEPTIDE
 <222> (7)..(8)
 <223> Val or non-natural derivatives of the aliphatic amino acid; Xaa at residue 8 is Lys, Arg, homolysine, homoarginine, ornithine, nor-Lys, His, N-methyl-Lys, N,N'-dimethyl-Lys, N,N',N''-trimethyl-Lys,

<220>
 <221> PEPTIDE
 <222> (8)..(9)
 <223> any synthetic basic amino acid, Ser, Thr, g-Ser, g-Thr or any hydroxylated synthetic residue; Xaa at residue 9 is an aliphatic amino acids bearing linear or branched saturated hydrocarbon chains such

<220>
 <221> PEPTIDE
 <222> (9)
 <223> as Leu (D or L), Ile and Val or non-natural derivatives of the aliphatic amino acid, Met, Phe, Tyr, meta-Tyr, ortho-Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr,

<220>
 <221> PEPTIDE
 <222> (9)..(11)
 <223> Trp (D or L), neo-Trp, halo-Trp (D or L) or any synthetic aromatic amino acid; Xaa at residue 11 is His, Ser, Thr, g-Ser, g-Thr, an aliphatic amino acid bearing linear or branched saturated

<220>
 <221> NP_BIND
 <222> (11)
 <223> hydrocarbon chains such as Leu (D or L), Ile and Val, non-natural derivatives of the aliphatic amino acid, Phe, Tyr, meta-Tyr, ortho-Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,

<220>
 <221> PEPTIDE
 <222> (11)..(14)
 <223> O-phospho-Tyr, nitro-Tyr, Trp (D or L), neo-Trp, halo-Trp (D or L) or a synthetic aromatic amino acid; Xaa at residue 12 is Pro, hydroxy- Pro (Hyp) or g-Hyp; Xaa at residue 14 is des-Xaa, Gly, Ala,

<220>
 <221> PEPTIDE
 <222> (14)
 <223> Lys, Arg, homolysine, homoarginine, ornithine, nor-Lys, His, N-methyl-Lys, N,N'-dimethyl-Lys, N,N',N''-trimethyl-Lys or any synthetic basic amino acid.

<400> 1
 Xaa Xaa Xaa Cys Cys Gly Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa
 1 5 10

<210> 2
 <211> 13
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (7)..(8)
 <223> Xaa at residue 7 is Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-Phospho-Tyr or nitro-Tyr; Xaa at residue 8 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl Lys

<220>
 <221> PEPTIDE
 <222> (12)
 <223> Xaa at residue 12 is Pro or hydroxy-Pro.

<400> 2
 Asn Gly Val Cys Cys Gly Xaa Xaa Leu Cys His Xaa Cys
 1 5 10

<210> 3
 <211> 12
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (6)..(7)
 <223> Xaa at residue 6 is Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-Phospho-Tyr or nitro-Tyr; Xaa at residue 7 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl Lys

<220>
 <221> PEPTIDE
 <222> (11)
 <223> Xaa at residue 11 is Pro or hydroxy-Pro

<400> 3
 Gly Val Cys Cys Gly Xaa Xaa Leu Cys His Xaa Cys
 1 5 10

<210> 4
 <211> 12
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism:unknown Conus species

<220>
 <221> PEPTIDE
 <222> (6)..(7)
 <223> Xaa at residue 6 is Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-Phospho-Tyr or nitro-Tyr; Xaa at residue 8 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl Lys.

<220>
 <221> PEPTIDE
 <222> (11)
 <223> Xaa at residue 11 is Pro or hydroxy-Pro

<400> 4
 Gly Val Cys Cys Gly Xaa Xaa Leu Cys His Xaa Cys
 1 5 10

<210> 5
 <211> 11
 <212> PRT
 <213> Conus bandanus

<220>
 <221> PEPTIDE
 <222> (5)..(6)
 <223> Xaa at residue 5 is Tyr, mono-halo-Tyr,
 di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
 nitro-Tyr; Xaa at residue 6 is Lys, N-methy-Lys,
 N,N-dimethyl-Lys or N,N,N-trimethyl-Lys;

<220>
 <221> PEPTIDE
 <222> (10)
 <223> Xaa at residue 10 is Pro or hydroxy-Pro (Hyp)

<400> 5
 Ala Cys Cys Gly Xaa Xaa Lys Cys Ser Xaa Cys
 1 5 10

<210> 6
 <211> 13
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(11)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at
 residue 6 is Tyr, mono-halo-Tyr, di-halo-Tyr,
 O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr; Xaa at
 residue 11 is Pro or hydroxy-Pro (Hyp)

<400> 6
 Xaa Thr Cys Cys Gly Xaa Arg Met Cys Val Xaa Cys Gly
 1 5 10

<210> 7
 <211> 13
 <212> PRT
 <213> Conus pennaceus

<220>
 <221> PEPTIDE
 <222> (7)..(11)
 <223> Xaa at residue 7 is Lys, N-methy-Lys,
 N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa at
 residue 11 is Pro or hydroxy-Pro (Hyp)

<400> 7

Ser Thr Cys Cys Gly Phe Xaa Met Cys Ile Xaa Cys Arg
 1 5 10

<210> 8
 <211> 25
 <212> DNA
 <213> Conus marmoreus

<220>
 <221> modified_base
 <222> (14)
 <223> i

<400> 8
 caggatccaa yggngtbtgy tgygg 25

<210> 9
 <211> 28
 <212> DNA
 <213> Conus marmoreus

<220>
 <221> modified_base
 <222> (26)
 <223> i

<400> 9
 ctg gatccgg rtgrcavary ttrtance 28

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:universal
 primer

<400> 10
 aagctcgagt aacaacgcag agt 23

<210> 11
 <211> 805
 <212> DNA
 <213> Conus marmoreus

<220>
 <221> CDS
 <222> (82)..(264)

<400> 11
 ggcgaataca cctggcaggt actcaacgaa cttcaggaca cattcttttc acctggacac 60
 tggaaactga caacaggcag a atg cgc tgt ctc cca gtc ttg atc att ctt 111
 Met Arg Cys Leu Pro Val Leu Ile Ile Leu
 1 5 10

ctg ctg ctg act gca tct gca cct ggc gtt gtt gtc cta ccg aag acc 159
 Leu Leu Leu Thr Ala Ser Ala Pro Gly Val Val Val Leu Pro Lys Thr
 15 20 25

cgaactgtcc	ctggatgtga	aatttgga	gcagactgtt	ccttttcgcac	gtattcgtgg	364
aatttcgaat	ggtcgtaaac	aacacgctgc	cacttgcagg	ctactatctc	tctgtccttt	424
catctgtgga	aatggatgat	ctaacaactg	aaatatcaga	aattttttcaa	tggctataca	484
ctatgaccat	gtagtcagta	attatatcat	ttggaccttt	tgaaatat	ttcaatatgt	544
aaagtgtttg	caccctggaa	aggtcttttg	gagttaaata	ttttagtatg	ttatgttttg	604
catacaagtt	atagaatgct	gtctttcttt	ttgttccac	atcaatggtg	ggggcagaaa	664
ttatttgttt	tggccaatgt	aattatgacc	tgcatttagt	gctatagtga	ttgcattttc	724
agcgtggaat	gtttaatctg	caaacagaaa	gtggttgatc	gactaataaa	gatttgcattg	784
gcacaaaaaa	aaaaaaaaaa	a				805

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<210> 12
<211> 61
<212> PRT
<213> Conus marmoreus
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<400> 12
Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser
  1              5              10              15

Ala Pro Gly Val Val Val Leu Pro Lys Thr Glu Asp Asp Val Pro Met
      20              25              30

Ser Ser Val Tyr Gly Asn Gly Lys Ser Ile Leu Arg Gly Ile Leu Arg
      35              40              45

Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys His Pro Cys
      50              55              60

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<210> 13
<211> 202
<212> DNA
<213> Conus bandanus
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<220>  
<221> CDS  
<222> (1) .. (183)
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<400> 13
atg cgc tgt ctc cca gtc ttg atc att ctt ctg ctg ctg act gca tct 48
Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15

gca cct ggc gtt gat gtc cta ccg aag acc gaa gat gat gtg ccc ctg 96
 Ala Pro Gly Val Asp Val Leu Pro Lys Thr Glu Asp Asp Val Pro Leu
 20 25 30

tca tct gtc tac gat aat aca aag agt atc cta cga gga ctt ctg gac 144
 Ser Ser Val Tyr Asp Asn Thr Lys Ser Ile Leu Arg Gly Leu Leu Asp
 35 40 45

aaa cgt gct tgc tgt ggc tac aag ctt tgc tca cca tgt taaccagcat 193
 Lys Arg Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys
 50 55 60

gaaggatcc 202

<210> 14
 <211> 61
 <212> PRT
 <213> Conus bandanus

<400> 14
 Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

Ala Pro Gly Val Asp Val Leu Pro Lys Thr Glu Asp Asp Val Pro Leu
 20 25 30

Ser Ser Val Tyr Asp Asn Thr Lys Ser Ile Leu Arg Gly Leu Leu Asp
 35 40 45

Lys Arg Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys
 50 55 60

<210> 15
 <211> 205
 <212> DNA
 <213> Conus textile

<220>
 <221> CDS
 <222> (1)..(186)

<400> 15
 atg cac tgt ctc cca atc ttc gtc att ctt ctg ctg ctg act gca tct 48
 Met His Cys Leu Pro Ile Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

gga cct agc gtt gat gcc caa ctg aag acc aaa gat gat gtg ccc ctg 96
 Gly Pro Ser Val Asp Ala Gln Leu Lys Thr Lys Asp Asp Val Pro Leu
 20 25 30

tca tct ttc cga gat cat gca aag agt acc cta cga aga ctt cag gac 144
 Ser Ser Phe Arg Asp His Ala Lys Ser Thr Leu Arg Arg Leu Gln Asp
 35 40 45

aaa cag act tgc tgt ggc tat agg atg tgt gtt cct tgt ggt 186
 Lys Gln Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys Gly
 50 55 60

taaccagcat gaaggatcc 205

<210> 16

<211> 62
 <212> PRT
 <213> Conus textile

<400> 16
 Met His Cys Leu Pro Ile Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15
 Gly Pro Ser Val Asp Ala Gln Leu Lys Thr Lys Asp Asp Val Pro Leu
 20 25 30
 Ser Ser Phe Arg Asp His Ala Lys Ser Thr Leu Arg Arg Leu Gln Asp
 35 40 45
 Lys Gln Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys Gly
 50 55 60

<210> 17
 <211> 211
 <212> DNA
 <213> Conus pennaceus

<220>
 <221> CDS
 <222> (1)..(189)

<400> 17
 atg cgc tgt ctc cca gtc ttc gtc att ctt ctg ctg ctg act gca tct 48
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15
 gca cct agc gtt gat gcc aaa gtt cat ctg aag acc aaa ggt gat ggg 96
 Ala Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly
 20 25 30
 ccc ctg tca tct ttc cga gat aat gca aag agt acc cta caa aga ctt 144
 Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu
 35 40 45
 cag gac aaa agc act tgc tgt ggc ttt aag atg tgt att cct tgt 189
 Gln Asp Lys Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys
 50 55 60
 cgттаaccag catgaaggat cc 211

<210> 18
 <211> 63
 <212> PRT
 <213> Conus pennaceus

<400> 18
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15
 Ala Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly
 20 25 30
 Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu
 35 40 45
 Gln Asp Lys Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys
 50 55 60

<210> 19
<211> 24
<212> DNA
<213> *Conus marmoreus*

<400> 19
ggaattcgga agctgactac aagc

24

<210> 20
<211> 22
<212> DNA
<213> *Conus marmoreus*

<400> 20
ctggatcctt catgctggtt aa

22